

AMENDMENTS TO THE CLAIMS

1. (Currently amended) A method for identifying a series of characteristics of a molecule comprising the steps of:

(i) converting the characteristics of the molecule into a polynucleotide of defined sequence, wherein each characteristic is represented by at least one distinct unit on the polynucleotide, ~~the unit comprising at least a single base; and wherein each unit on the polynucleotide comprises two or three of the different bases A, T(U), G and C, one of which represents a target for the subsequent incorporation of a detectably labelled nucleotide, and one which represents a stop signal;~~

(ii) contacting the polynucleotide with at least one of the nucleotides dATP, dTTP (dUTP), dGTP and dCTP, under conditions that permit the polymerisation reaction to proceed, wherein the at least one nucleotide comprises a detectable label specific for the nucleotide;

(iii) removing any non-incorporated nucleotides and detecting any incorporation events;

(iv) removing any labels; and

(v) repeating steps (ii) to (iv) to thereby identify the different units, and thereby the characteristics of the molecule,

wherein the molecule is a target polynucleotide, and wherein the characteristic to be identified is the partial or complete sequence of the target polynucleotide.

2. (Currently amended) A method according to claim 1, ~~wherein each unit on the polynucleotide comprises two or three of the different bases A, T(U), G and C, one of which represents a target for the subsequent incorporation of the detectably labelled nucleotide, and one represents a stop signal, and~~ wherein step (ii) is carried out in the presence of nucleotides complementary to the bases of the unit but in the absence of a nucleotide complementary to that of the stop signal.

3. (Original) A method according to claim 1 or claim 2, wherein consecutive units on the polynucleotide have a different base type as the target for the incorporation of a labelled nucleotide.

4. (Previously Presented) A method according to claim 1, wherein each unit comprises two bases of the same type as targets for the incorporation of labelled nucleotides.

5-6. (Canceled)

7. (Previously Presented) A method according to claim 1, wherein the label is a fluorophore.

8. (Currently amended) A method according to claim 7, wherein the fluorophore is ~~Alexa-red~~ Alexa-647 or ~~Alexa-green~~ Alexa-488.

9. (Previously Presented) A method according to claim 1, wherein the polynucleotide of step (i) is immobilised on a support material.

10. (Original) A method according to claim 9, wherein the immobilised polynucleotide forms an array on the support material, the array having a density that permits individual resolution of a detectable label.

11. (Previously Presented) A method according to claim 1, wherein detection is carried out by optical microscopy.

12. (Previously Presented) A method according to claim 5, wherein each of the bases A, T(U), G and C on the target polynucleotide is represented by a combination of two sequential units, with each base represented by a different combination of the two units.

13-16. (Canceled)

17. (Previously Presented) A method according to claim 4, wherein the two bases are separated by one or more of a third base of a different type.

18. (New) A method for identifying nucleotide sequence characteristics of a target polynucleotide, comprising:

(i) converting the target polynucleotide into a new polynucleotide, wherein each characteristic of the target polynucleotide comprises on the new polynucleotide a unit that comprises two or three of the different bases A, T(U), G and C, one of which represents a target for the subsequent incorporation of a detectably labelled nucleotide, and one which represents a stop signal;

(ii) contacting the target polynucleotide with at least one of the nucleotides dATP, dTTP (dUTP), dGTP and dCTP, under conditions that permit a polymerisation reaction to proceed, wherein the at least one nucleotide comprises a detectable label specific for the nucleotide;

(iii) removing any non-incorporated nucleotides and detecting any incorporation events;

(iv) removing any labels; and

(v) repeating steps (ii) to (iv) to thereby identify the different units, and thereby the sequence characteristics of the molecule.